**Figure 1a**

Atgcagaaggaagtggagcagaactctggacccctcagtgttccagagggagccatt
gcctctctcaactgcacttacagtgaccgaggttcccagtccttcttctggtacaga
caatattctgggaaaagccctgagttgataatgtccatatactccaatggtgacaaa
gaagatggaaggtttacagcacagctcaataaagccagccagtatgtttctctgctc
atcagagactcccagcccagtgattcagccacctacctctgtgccgttacaactgac
agctgggggaaattgcagtttggagcagggacccaggttgtggtcaccccagatatc
cagaaccctgaccctgccgtgtaccagctgagagactctaaatccagtgacaagtct
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gatgtgtatatcacagacaaatggtgtgctagacatgaggtctatggacttcaagagc
aacagtgctgtggcctggagcaacaaatctgactttgcatgtgcaaacgccttcaac
aacagcattattccagaagacaccttcttccccagcccagaaagttcctaa

**(SEQ ID 147)**

**Figure 1b**

atgaacgctggtgtcactcagaccccaaaattccaggtcctgaagacaggacagagc
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gacccaggcatggggctgaggctgattcattactcagttggtgctggtatcactgac
caaggagaagtccccaatggctacaatgtctccagatcaaccacagaggatttcccg
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ccgggactagcgggagggcgaccagagcagtacttcgggccgggcaccaggctcacg
gtcacagaggacctgaaaaacgtgttcccacccgaggtcgctgtgtttgagccatca
gaagcagagatctcccacacccaaaaggccacactggtgtgcctggccacaggcttc
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gctctgagcagccgcctgagggtctcggccaccttctggcaggacccccgcaaccac
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agggccaaacccgtcacccagatcgtcagcgccgaggcctggggtagagcagactaa

**(SEQ ID 148)**

**Figure 2a**

MQ
KEVEQNSGPL SVPEGAIASL NCTYSDRGSQ SFFWYRQYSG KSPELIMSIY
SNGDKEDGRF TAQLNKASQY VSLLIRDSQP SDSATYLCAV TTDSWGKLQF
GAGTQVVVTP DIQNPDPAVY QLRDSKSSDK SVCLFTDFDS QTNVSQSKDS
DVYITDKCVL DMRSMDFKSN SAVAWSNKSD FACANAFNNS IIPEDTFFPS
PESS*
**(SEQ ID 149)**

**Figure 2b**

M
NAGVTQTPKF QVLKTGQSMT LQCAQDMNHE YMSWYRQDPG MGLRLIHYSV
GAGITDQGEV PNGYNVSRST TEDFPLRLLS AAPSQTSVYF CASRPGLAGG
RPEQYFGPGT RLTVTEDLKN VFPPEVAVFE PSEAEISHTQ KATLVCLATG
FYPDHVELSW WVNGKEVHSG VCTDPQPLKE QPALNDSRYA LSSRLRVSAT
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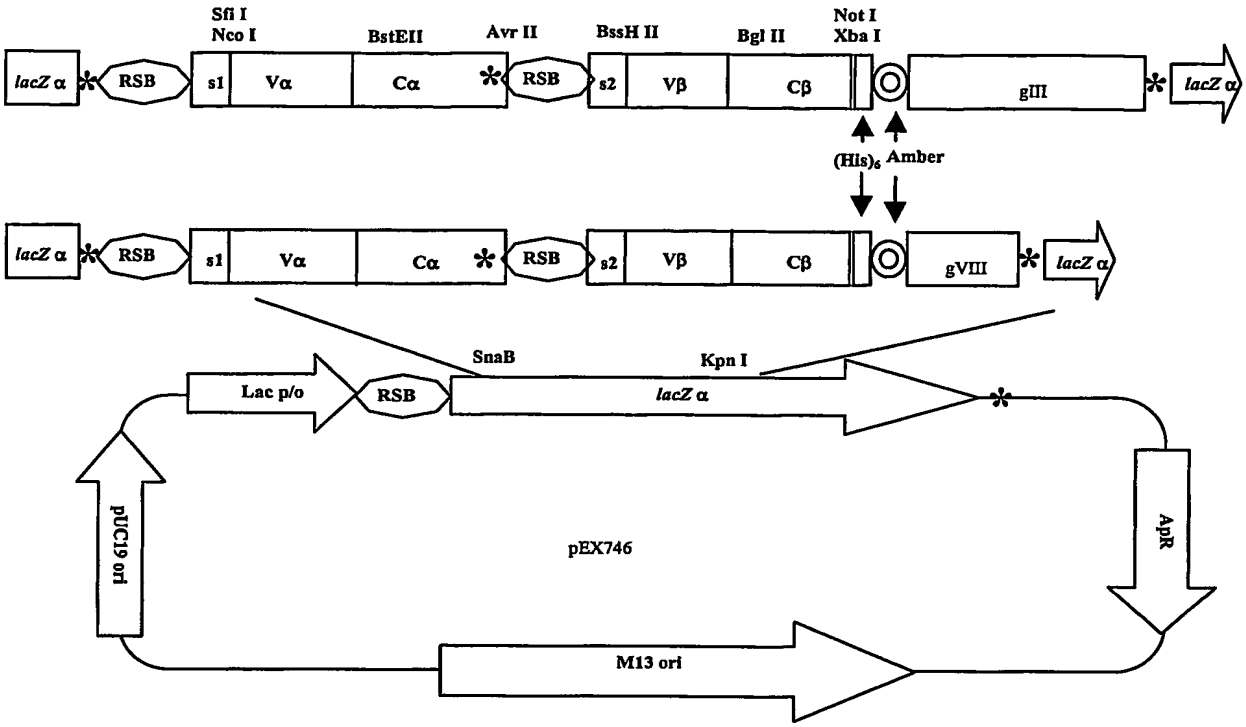
**(SEQ ID 150)**

**Figure 3**


Sfi I
Nco I
BstEII
Avr II
BssH II
Bgl II
Not I
Xba I
lacZ α
RSB
s1
Vα
Cα
RSB
s2
Vβ
Cβ
gIII
lacZ α
(His)6
Amber
lacZ α
RSB
s1
Vα
Cα
RSB
s2
Vβ
Cβ
gVIII
lacZ α
SnaB
Kpn I
Lac p/o
RSB
lacZ α
pUC19 ori
pEX746
ApR
M13 ori

## Figure 4

```
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 121 ataatattga aaaaggaaga gtatgagtat tcaacatttc cgtgtcgccc ttattccctt
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 301 gatccttgag agttttcgcc ccgaagaacg ttctccaatg atgagcactt ttaaagttct
 361 gctatgtggc gcggtattat cccgtgttga cgccgggcaa gagcaactcg gtcgccgcat
 421 acactattct cagaatgact tggttgagta ctcaccagtc acagaaaagc atcttacgga
 481 tggcatgaca gtaagagaat tatgcagtgc tgccataacc atgagtgata acactgcggc
 541 caacttactt ctgacaacga tcggaggacc gaaggagcta accgcttttt tgcacaacat
 601 gggggatcat gtaactcgcc ttgatcgttg ggaaccggag ctgaatgaag ccataccaaa
 661 cgacgagcgt gacaccacga tgcctgtagc aatggcaaca acgttgcgca aactattaac
 721 tggcgaacta cttactctag cttcccggca acaattaata gactggatgg aggcggataa
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 841 tggagccggt gagcgtgggt ctcgcggtat cattgcagca ctggggccag atggtaagcc
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1201 aaatcaaaag aatagcccga gatagggttg agtgttgttc cagtttggaa caagagtcca
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2161 gcctggtatc tttatagtcc tgtcgggttt cgccacctct gacttgagcg tcgatttttg
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5341 tacccaactt aatcgccttg cagcacatcc ccctttcgcc agctggcgta atagcgaaga
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**(SEQ ID 151)**

**Figure 5**

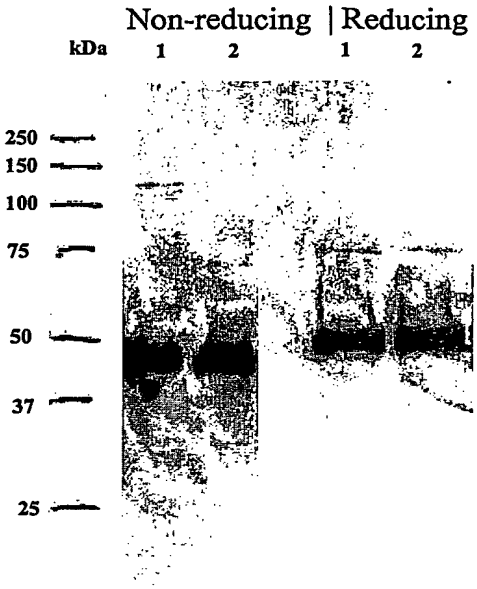
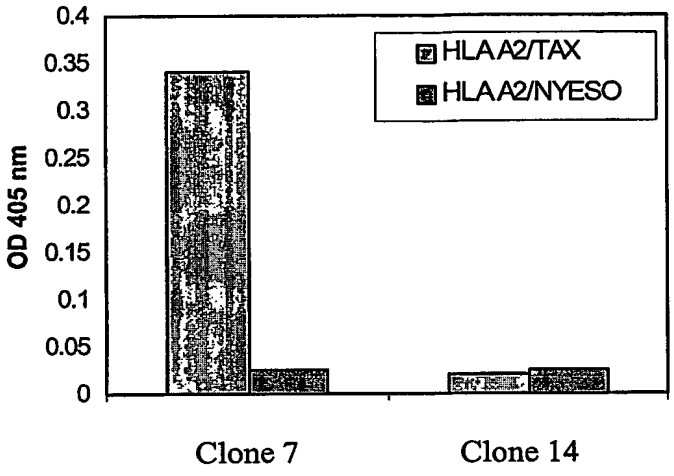


**Figure 6**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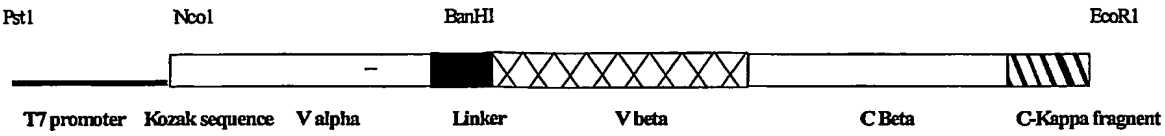
0.3
0.25
0.2
0.15
0.1
0.05
0
OD 405 nm
HLA A2/TAX
HLA A2/NYESO
Clone 7
Clone 14

## Figure 7a

Schematic diagram of the A6 scTCR-C-Kappa ribosome display construct




## Figure 7b

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tacagacaat attctgggaa aagccctgag ttgataatgt ccatatactc

caatggtgac aaagaagatg gaaggtttac agcacagctc aataaagcca

gccagtatgt ttctctgctc atcagagact cccagcccag tgattcagcc

acctacctct gtgccgttac aactgacagc tgggggaaat tgcagtttgg

agcagggacc caggttgtgg tcaccggtgg aggcggttca ggcggaggtg

gatccggcgg tggcgggtcg aacgctggtg tcactcagac cccaaaattc

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gaaccatgaa tacatgtcct ggtatcgaca agacccaggc atggggctga

ggctgattca ttactcagtt ggtgctggta tcactgacca aggagaagtc

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aggctcacgg tcacagagga cctgaaaaac gtgttcccac ccgaggtcgc

tgtgtttgag ccatcagaag cagagatctc ccacacccaa aaggccacac

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cag

**(SEQ ID 152)**

**Figure 7C**

| | | | | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| M | G | Q | K | E | V | E | Q | N | S | G | P | L | S | V | P | E | G | A | I | A | S | L |
| N | C | T | Y | S | D | R | G | S | Q | S | F | F | W | Y | R | Q | Y | S | G | K | S | P |
| E | L | I | M | S | I | Y | S | N | G | D | K | E | D | G | R | F | T | A | Q | L | N | K |
| A | S | Q | Y | V | S | L | L | I | R | D | S | P | S | D | S | A | T | Y | L | C | A | V |
| T | T | D | S | W | G | K | L | Q | F | G | A | G | T | Q | V | V | V | T | G | G | G | G |
| S | G | G | G | G | S | G | G | G | G | S | N | A | G | V | T | Q | T | P | K | F | Q | V |
| L | K | T | G | Q | S | M | T | L | Q | C | A | Q | D | M | N | H | E | Y | M | S | W | Y |
| R | Q | D | P | G | M | G | L | R | L | I | H | Y | S | V | G | A | G | I | T | D | Q | G |
| E | V | P | N | G | Y | N | V | S | R | S | T | T | E | D | F | P | L | R | L | L | S | A |
| A | P | S | Q | T | S | V | Y | F | C | A | S | R | P | G | L | A | G | G | R | P | E | Q |
| Y | F | G | P | G | T | R | L | T | V | T | E | D | L | K | N | V | F | P | P | E | V | A |
| V | F | E | P | S | E | A | E | I | S | H | T | Q | K | A | T | L | V | C | L | A | T | G |
| F | Y | P | D | H | V | E | L | S | W | W | V | N | G | K | E | V | H | S | G | V | S | T |
| D | P | Q | P | L | K | E | Q | P | A | L | N | D | S | R | Y | A | L | S | S | R | L | R |
| V | S | A | T | F | W | Q | D | P | R | N | H | F | R | C | Q | V | Q | F | Y | G | L | S |
| E | N | D | E | W | T | Q | D | R | A | K | P | V | T | Q | I | V | S | A | E | A | W | G |
| R | A | D | G | G | G | G | S | L | S | S | T | L | T | L | S | K | A | D | Y | E | K | H |
| K | V | Y | A | C | E | V | T | H | Q | G | L | S | S | P | V | T | K | S | F | N | R | G |
| E | S | | | | | | | | | | | | | | | | | | | | | |

**(SEQ ID: 153)**

# Figure 8

pUC19-T7 sequence

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1961 ttgctggctc gcgtcgctca gtcactcgct ccttcgcctt ctcgcgggtt atgcgtttgg cggagagggg
2031 cgcgcaaccg gctaagtaat tacgtcgacc gtgctgtcca aagggctgac ctttcgcccg tcactcgcgt
2101 tgcgttaatt acactcaatc gagtgagtaa tccgtggggt ccgaaatgtg aaatacgaag gccgagcata
2171 caacacacct taacactcgc ctattgttaa agtgtgtcct ttgtcgatac tggtactaat gcggttcgac
2241 gtcgattatg ctgagtgata tccttgtccg gtggtaccct aggggcccat ggctcgagct taagtgaccg
2311 gcagcaaaat gttgcagcac tgacccтttt gggaccgcaa tgggttgaat tagcggaacg tcgtgtaggg
2381 ggaaagcggt cgaccgcatt atcgcttctc cgggcgtggc tagcgggaag ggttgtcaac gcgtcggact
2451 taccgcttac cgcggactac gccataaaag aggaatgcgt agacacgcca taaagtgtgg cgtataccac
2521 gtgagagtca tgttagacga gactacggcg tatcaattcg gtcggggctg tgggcggttg tgggcgactg
2591 cgcgggactg cccgaacaga cgagggccgt aggcgaatgt ctgttcgaca ctggcagagg ccctcgacgt
2661 acacagtctc caaaagtggc agtagtggct ttgcgcgct
```

**(SEQ ID 154)**

**Figure 9**

A6 scTCR-C-kappa cloned into pUC19-T7

```
   1 ccatgggcca gaaggaagtg gagcagaact ctggacccct cagtgttcca
  51 gagggagcca ttgcctctct caactgcact tacagtgacc gaggttccca
 101 gtccttcttc tggtacagac aatattctgg gaaaagccct gagttgataa
 151 tgtccatata ctccaatggt gacaaagaag atggaaggtt tacagcacag
 201 ctcaataaag ccagccagta tgtttctctg ctcatcagag actcccagcc
 251 cagtgattca gccacctacc tctgtgccgt tacaactgac agctggggga
 301 aattgcagtt tggagcaggg acccaggttg tggtcaccgg tggaggcggt
 351 tcaggcggag gtggatccgg cggtggcggg tcgaacgctg gtgtcactca
 401 gaccccaaaa ttccaggtcc tgaagacagg acagagcatg acactgcagt
 451 gtgcccagga tatgaaccat gaatacatgt cctggtatcg acaagaccca
 501 ggcatggggc tgaggctgat tcattactca gttggtgctg gtatcactga
 551 ccaaggagaa gtccccaatg gctacaatgt ctccagatca accacagagg
 601 atttcccgct caggctgctg tcggctgctc cctcccagac atctgtgtac
 651 ttctgtgcca gcaggccggg actagcggga gggcgaccag agcagtactt
 701 cgggccgggc accaggctca cggtcacaga ggacctgaaa aacgtgttcc
 751 cacccgaggt cgctgtgttt gagccatcag aagcagagat ctcccacacc
 801 caaaaggcca cactggtgtg cctggccaca ggcttctacc ccgaccacgt
 851 ggagctgagc tggtgggtga atgggaagga ggtgcacagt ggggtcagca
 901 cagacccgca gccctcaag gagcagcccg ccctcaatga ctccagatac
 951 gctctgagca gccgcctgag ggtctcggcc accttctggc aggacccccg
1001 caaccacttc cgctgtcaag tccagttcta cgggctctcg gagaatgacg
1051 agtggaccca ggatagggcc aaacccgtca cccagatcgt cagcgccgag
1101 gcctggggta gagcagacgg tggaggcggt tcactcagca gcaccctgac
1151 gctgagcaaa gcagactacg agaaacacaa agtctacgcc tgcgaagtca
1201 cccatcaggg cctgagttcg cccgtcacaa agagcttcaa ccgcggagag
1251 tcataagaat tc
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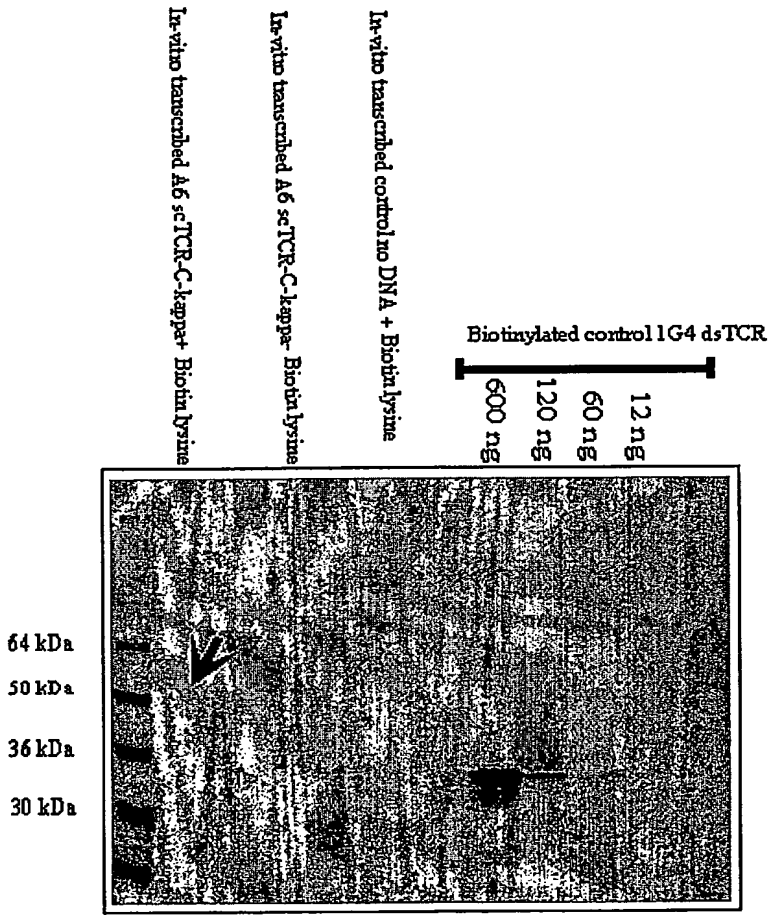
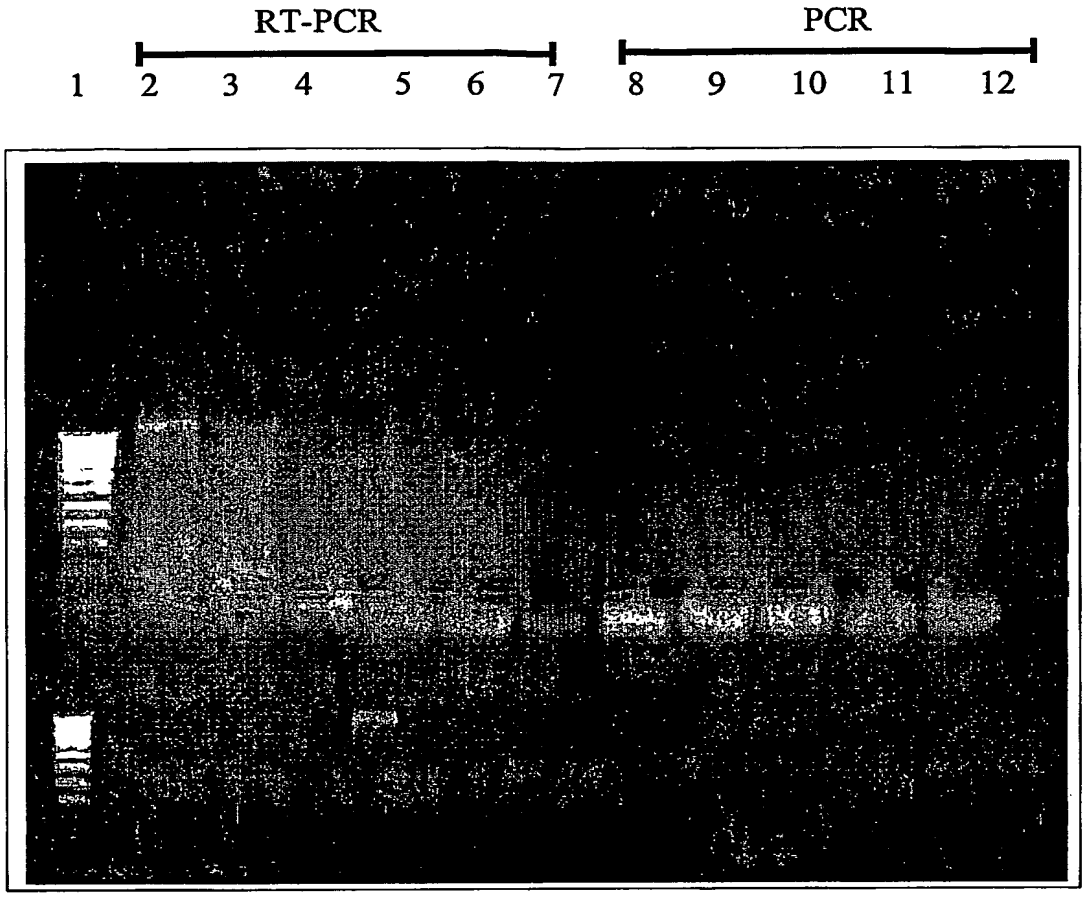
**(SEQ ID 155)**

## Figure 10




The A6 scTCR-C-Kappa protein is shown in the above western blot with an arrow.

**Figure 11**




Lane 1 Bioline 100bp DNA marker
Lane 2 A6scTCR-C-Kappa reaction selected againt HLA-A2 TAX beads
Lane 3 A6scTCR-C-Kappa reaction selected againt HLA-A2 TAX beads in the presence of 10 microgrammes of soluble A6scTCR
Lane 4 A6scTCR-C-Kappa reaction selected againt control beads
Lane 5 Control no DNA reaction selected against HLA-A2-TAX beads
Lane 6 Control no DNA reaction selected againt HLA-A2 TAX beads in the presence of 10 microgrammes of soluble A6scTCR
Lane 7 Control no DNA reaction selected againt control beads
Lanes 8-12 and lane 13 are as lanes 2-7 except no rerverse transcriptase was added just Roche high fidelity taq. These are the DNA contamination controls.
Lane 13 RT-PCR positive control.

**Figure 12a**

Clone 9 Mutated A6 TCR β chain DNA sequence

gctggtgtcactcagaccccaaaattccaggtcctgaagacaggacagagcatgacactgcagtgtgcccaggatatgaaccat
gaatacatgtcctggtatcgacaagacccaggcatggggctgaggctgattcattactcagttggtgctggtatcactgaccaagga
gaagtccccaatggctacaatgtctccagatcaaccacagaggatttcccgctcaggctgctgtcggctgctccctcccagacatct
gtgtacttctgtgccagcaggccgggactagcgggagggtgaccagagcagtacttcgggccgggcaccaggctcacggtcac
agaggacctgaaaaacgtgttcccacccgaggtcgctgtgtttgagccatcagaagcagagatctcccacacccaaaaggcca
cactggtgtgcctggccacaggcttctaccccgaccacgtggagctgagctggtgggtgaatgggaaggaggtgcacagtgggg
tctgcacagacccgcagcccctcaaggagcagcccgccctcaatgactccagatacgctctgagcagccgcctgagggtctcgg
ccaccttctggcaggacccccgcaaccacttccgctgtcaagtccagttctacgggctctcggagaatgacgagtggacccagga
tagggccaaacccgtcacccagatcgtcagcgccgaggcctggggtagagcagac

**(SEQ ID 156)**

**Figure 12b**

Clone 9 Mutated A6 TCR β chain amino acid sequence

AGVTQTPKFQVLKTGQSMTLQCAQDMNHEYMSWYRQDPGMGLRLIHYSVGAGITDQGEVP
NGYNVSRSTTEDFPLRLLSAAPSQTSVYFCASRPGLAGGXPEQYFGPGTRLTVTEDLKNVF
PPEVAVFEPSEAEISHTQKATLVCLATGFYPDHVELSWWVNGKEVHSGVCTDPQPLKEQPA
LNDSRYALSSRLRVSATFWQDPRNHFRCQVQFYGLSENDEWTQDRAKPVTQIVSAEAWGR
AD

**(SEQ ID 157)**

X - Denotes the position of the amino acid corresponding to the introduced 'opal' stop codon, this will generally result in the substitution of a tryptophan (w) residue into the TCR β chain at this point.

**Figure 13**

Clone 49 Mutated A6 TCR β chain DNA sequence

gctggtgtcactcagaccccaaaattccaggtcctgaagacaggacagagcatgacactgtagtgtgcccaggatatgaaccat
gaatacatgtcctggtatcgacaagacccaggcatggggctgaggctgattcattactcagttggtgctggtatcactgaccaagga
gaagtccccaatggctacaatgtctccagatcaaccacagaggatttcccgctcaggctgctgtcggctgctccctcccagacatct
gtgtacttctgtgccagcaggccgggactagcgggagggcgaccagagcagtacttcgggccgggcaccaggctcacggtcac
agaggacctgaaaaacgtgttcccacccgaggtcgctgtgtttgagccatcagaagcagagatctcccacacccaaaaggcca
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tctgcacagacccgcagcccctcaaggagcagcccgccctcaatgactccagatacgctctgagcagccgcctgagggtctcgg
ccaccttctggcaggacccccgcaaccacttccgctgtcaagtccagttctacgggctctcggagaatgacgagtggacccagga
tagggccaaacccgtcacccagatcgtcagcgccgaggcctggggtagagcagac

**(SEQ ID 158)**

**Figure 14a**

Clone 134 Mutated A6 TCR β chain DNA sequence

gctggtgtcactcagaccccaaaattccaggtcctgaagacaggacagagcatgacactgcagtgtgcccaggatatgaaccat
gaatacatgtcctggtatcgacaagacccaggcatggggctgaggctgattcattactcagttggtgctggtatcactgaccaagga
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gtgtacttctgtgcctcgaggccggggctg**atgagtgcggaa**ccagagcagtacttcgggccgggcaccaggctcacggtcac
agaggacctgaaaaacgtgttcccacccgaggtcgctgtgtttgagccatcagaagcagagatctcccacacccaaaaggcca
cactggtgtgcctggccaccggtttctaccccgaccacgtggagctgagctggtgggtgaatgggaaggaggtgcacagtggggt
ctgcacagacccgcagcccctcaaggagcagcccgccctcaatgactccagatacgctctgagcagccgcctgagggtctcgg
ccaccttctggcaggacccccgcaaccacttccgctgtcaagtccagttctacgggctctcggagaatgacgagtggacccagga
tagggccaaacccgtcacccagatcgtcagcgccgaggcctggggtagagcagactaagcttgaattc

**(SEQ ID 159)**

**Figure 14b**

Clone 134A Mutated A6 TCR β chain amino acid sequence (BIAcore)

MNAGVTQTPKFQVLKTGQSMTLQCAQDMNHEYMSWYRQDPGMGLRLIHYSVGAGITDQG
EVPNGYNVSRSTTEDFPLRLLSAAPSQTSVYFCASRPGL**MSAE**PEQYFGPGTRLTVTEDLK
NVFPPEVAVFEPSEAEISHTQKATLVCLATGFYPDHVELSWWVNGKEVHSGVCTDPQPLKE
QPALNDSRYALSSRLRVSATFWQDPRNHFRCQVQFYGLSENDEWTQDRAKPVTQIVSAEA
WGRAD*

**(SEQ ID 160)**

**Figure 14c**

Clone 134 Mutated A6 TCR β chain amino acid sequence (ELISA)

AGVTQTPKFQVLKTGQSMTLQCAQDMNHEYMSWYRQDPGMGLRLIHYSVGAGITDQGEVP
NGYNVSRSTTEDFPLRLLSAAPSQTSVYFCASRPGL**MSAQ**PEQYFGPGTRLTVTEDLKNVF
PPEVAVFEPSEAEISHTQKATLVCLATGFYPDHVELSWWVNGKEVHSGVCTDPQPLKEQPA
LNDSRYALSSRLRVSATFWQDPRNHFRCQVQFYGLSENDEWTQDRAKPVTQIVSAEAWGR
AD

**(SEQ ID 161)**

Figure 15

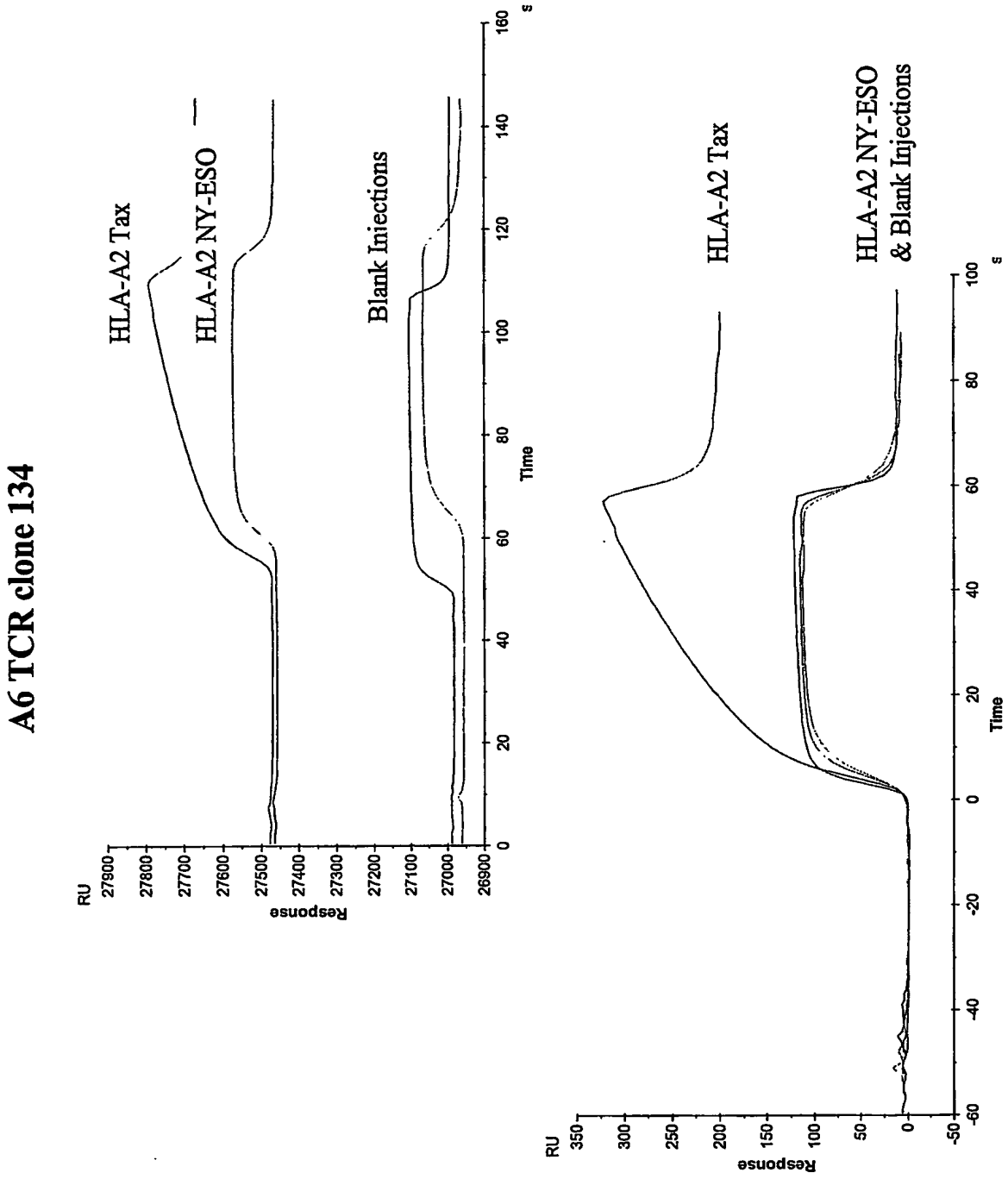
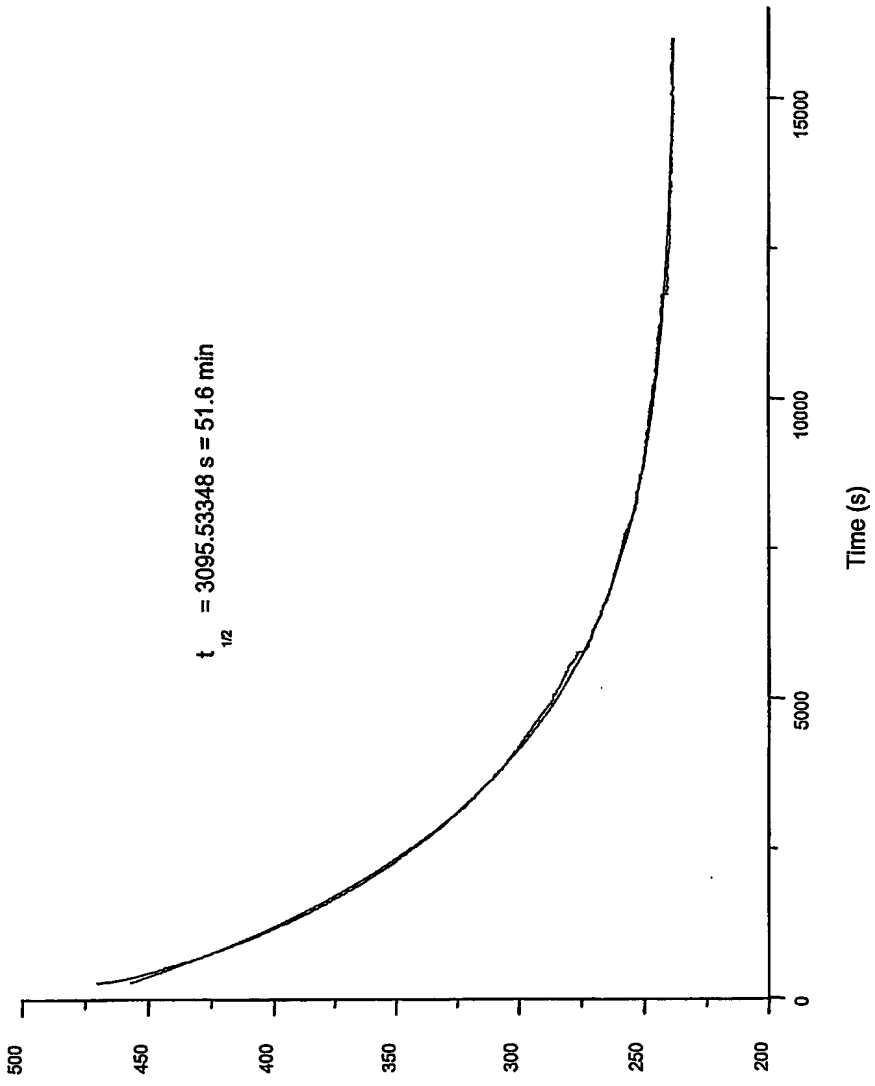

A6 TCR clone 134
HLA-A2 Tax
HLA-A2 NY-ESO
Blank Injections
RU
Response
Time
s
HLA-A2 Tax
HLA-A2 NY-ESO
& Blank Injections
RU
Response
Time
s

Figure 16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500
450
400
350
300
250
200
0
5000
10000
15000
Time (s)

**Figure 17a**

atgcaggaggtgacacagattcctgcagctctgagtgtcccagaaggagaaaacttggttctcaactgcagtttcactgata
gcgctatttacaacctccagtggtttaggcaggaccctgggaaaggtctcacatctctgttgcttattcagtcaagtcagaga
gagcaaacaagtggaagacttaatgcctcgctggataaatcatcaggacgtagtactttatacattgcagcttctcagcctgg
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gcattattccagaagacaccttcttccccagcccagaaagttcctaa
**(SEQ ID 162)**

**Figure 17b**

atgggtgtcactcagaccccaaaattccaggtcctgaagacaggacagagcatgacactgcagtgtgcccaggatatgaa
ccatgaatacatgtcctggtatcgacaagacccaggcatggggctgaggctgattcattactcagttggtgctggtatcactg
accaaggagaagtccccaatggctacaatgtctccagatcaaccacagaggatttcccgctcaggctgctgtcggctgctc
cctcccagacatctgtgtacttctgtgccagcagttacgtcgggaacaccggggagctgttttttggagaaggctctaggctg
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caaaaggccacactggtgtgcctggccacaggcttctaccccgaccacgtggagctgagctggtgggtgaatgggaagg
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ggagaatgacgagtggacccaggatagggccaaacccgtcacccagatcgtcagcgccgaggcctggggtagagcag
actaa
**(SEQ ID 163)**

**Figure 18a**

M Q E V T Q I P A A L S V P E G E N L V L N C S F T D S A I Y N L Q W F R Q
D P G K G L T S L L L I Q S S Q R E Q T S G R L N A S L D K S S G R S T L Y I
A A S Q P G D S A T Y L C A V R P T S G G S Y I P T F G R G T S L I V H P Y I
Q N P D P A V Y Q L R D S K S S D K S V C L F T D F D S Q T N V S Q S K D S
D V Y I T D K C V L D M R S M D F K S N S A V A W S N K S D F A C A N A F
N N S I I P E D T F F P S P E S S **Stop**
**(SEQ ID 164)**

**Figure 18b**

M G V T Q T P K F Q V L K T G Q S M T L Q C A Q D M N H E Y M S W Y R Q
D P G M G L R L I H Y S V G A G I T D Q G E V P N G Y N V S R S T T E D F P
L R L L S A A P S Q T S V Y F C A S S Y V G N T G E L F F G E G S R L T V L E
D L K N V F P P E V A V F E P S E A E I S H T Q K A T L V C L A T G F Y P D H
V E L S W W V N G K E V H S G V C T D P Q P L K E Q P A L N D S R Y A L S
S R L R V S A T F W Q D P R N H F R C Q V Q F Y G L S E N D E W T Q D R A
K P V T Q I V S A E A W G R A D **Stop (SEQ ID 165)**

## Figure 19a

TTCCTGGCCT TTTGCTGGCC TTTTGCTCAC ATGTAATGTG AGTTAGCTCA
AAGGACCGGA AAACGACCGG AAAACGAGTG TACATTACAC TCAATCGAGT
CTCATTAGGC ACCCCAGGCT TTACACTTTA TGCTTCCGGC TCGTATGTTG
GAGTAATCCG TGGGGTCCGA AATGTGAAAT ACGAAGGCCG AGCATACAAC
TGTGGAATTG TGAGCGGATA ACAATTTCAC ACAGGAAACA GCTATGACCA
ACACCTTAAC ACTCGCCTAT TGTTAAAGTG TGTCCTTTGT CGATACTGGT
TGATTACGCC AAGCTACGTA CTTAAGTATT CTATTTCAAG GAGACAGTCA
ACTAATGCGG TTCGATGCAT GAATTCATAA GATAAAGTTC CTCTGTCAGT
TAATGAAATA CCTATTGCCT ACGGCAGCCG CTGGATTGTT ATTACTCGCG
ATTACTTTAT GGATAACGGA TGCCGTCGGC GACCTAACAA TAATGAGCGC
GCCCAGCCGG CCATGGCCAA ACAGGAGGTG ACGCAGATTC CTGCAGCTCT
CGGGTCGGCC GGTACCGGTT TGTCCTCCAC TGCGTCTAAG GACGTCGAGA
GAGTGTCCCA GAAGGAGAAA ACTTGGTTCT CAACTGCAGT TTCACTGATA
CTCACAGGGT CTTCCTCTTT TGAACCAAGA GTTGACGTCA AAGTGACTAT
GCGCTATTTA CAACCTCCAG TGGTTTAGGC AGGACCCTGG GAAAGGTCTC
CGCGATAAAT GTTGGAGGTC ACCAAATCCG TCCTGGGACC CTTTCCAGAG
ACATCTCTGT TGCTTATTCA GTCAAGTCAG AGAGAGCAAA CAAGTGGAAG
TGTAGAGACA ACGAATAAGT CAGTTCAGTC TCTCTCGTTT GTTCACCTTC
ACTTAATGCC TCGCTGGATA AATCATCAGG ACGTAGTACT TTATACATTG
TGAATTACGG AGCGACCTAT TTAGTAGTCC TGCATCATGA AATATGTAAC
CAGCTTCTCA GCCTGGTGAC TCAGCCACCT ACCTCTGTGC TGTGAGGCCC
GTCGAAGAGT CGGACCACTG AGTCGGTGGA TGGAGACACG ACACTCCGGG
ACATCAGGAG GAAGCTACAT ACCTACATTT GGAAGAGGAA CCAGCCTTAT
TGTAGTCCTC CTTCGATGTA TGGATGTAAA CCTTCTCCTT GGTCGGAATA
TGTTCATCCG TATATCCAGA ACCCGGATCC TGCCGTGTAC CAGCTGAGAG
ACAAGTAGGC ATATAGGTCT TGGGCCTAGG ACGGCACATG GTCGACTCTC
ACTCTAAATC CAGTGACAAG TCTGTCTGCC TATTCACCGA TTTTGATTCT
TGAGATTTAG GTCACTGTTC AGACAGACGG ATAAGTGGCT AAAACTAAGA
CAAACAAATG TGTCACAAAG TAAGGATTCT GATGTGTATA TCACAGACAA
GTTTGTTTAC ACAGTGTTTC ATTCCTAAGA CTACACATAT AGTGTCTGTT
ATGTGTGCTA GACATGAGGT CTATGGACTT CAAGAGCAAC AGTGCTGTGG
TACACACGAT CTGTACTCCA GATACCTGAA GTTCTCGTTG TCACGACACC
CCTGGAGCAA CAAATCTGAC TTTGCATGTG CAAACGCCTT CAACAACAGC
GGACCTCGTT GTTTAGACTG AAACGTACAC GTTTGCGGAA GTTGTTGTCG
ATTATTCCAG AAGACACCTT CTTCCCCAGC CCAGAAAGTT CCTAATAACC
TAATAAGGTC TTCTGTGGAA GAAGGGGTCG GGTCTTTCAA GGATTATTGG
TAGGTTAATT AAGAATTCTT TAAGAAGGGG ATATACATAT GAAAAAATTA
ATCCAATTAA TTCTTAAGAA ATTCTTCCCC TATATGTATA CTTTTTTAAT
TTATTCGCAA TTCCTTTAGT TGTTCCTTTC TATTCTCACA GCGCGCAGGC
AATAAGCGTT AAGGAAATCA ACAAGGAAAG ATAAGAGTGT CGCGCGTCCG
TGGTGTCACT CAGACCCCAA AATTCCAGGT CCTGAAGACA GGACAGAGCA
ACCACAGTGA GTCTGGGGTT TTAAGGTCCA GGACTTCTGT CCTGTCTCGT
TGACACTGCA GTGTGCCCAG GATATGAACC ATGAATACAT GTCCTGGTAT
ACTGTGACGT CACACGGGTC CTATACTTGG TACTTATGTA CAGGACCATA
CGACAAGACC CAGGCATGGG GCTGAGGCTG ATTCATTACT CAGTTGGTGC
GCTGTTCTGG GTCCGTACCC CGACTCCGAC TAAGTAATGA GTCAACCACG
TGGTATCACT GACCAAGGAG AAGTCCCCAA TGGCTACAAT GTCTCCAGAT
ACCATAGTGA CTGGTTCCTC TTCAGGGGTT ACCGATGTTA CAGAGGTCTA
CAACCACAGA GGATTTCCCG CTCAGGCTGC TGTCGGCTGC TCCCTCCCAG
GTTGGTGTCT CCTAAAGGGC GAGTCCGACG ACAGCCGACG AGGGAGGGTC
ACATCTGTGT ACTTCTGTGC CAGCAGTTAC GTCGGGAACA CCGGGGAGCT
TGTAGACACA TGAAGACACG GTCGTCAATG CAGCCCTTGT GGCCCCTCGA
GTTTTTTGGA GAAGGCTCTA GGCTGACCGT ACTGGAGGAC CTGAAAAACG
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TGTTCCCACC CGAGGTCGCT GTGTTTGAGC CATCAGAAGC AGAGATCTCC
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CCACGTGGAG CTGAGCTGGT GGGTGAATGG GAAGGAGGTG CACAGTGGGG
GGTGCACCTC GACTCGACCA CCCACTTACC CTTCCTCCAC GTGTCACCCC
TCTGCACAGA CCCGCAGCCC CTCAAGGAGC AGCCCGCCCT CAATGACTCC
AGACGTGTCT GGGCGTCGGG GAGTTCCTCG TCGGGCGGGA GTTACTGAGG
AGATACGCTC TGAGCAGCCG CCTGAGGGTC TCGGCCACCT TCTGGCAGGA
TCTATGCGAG ACTCGTCGGC GGACTCCCAG AGCCGGTGGA AGACCGTCCT
CCCCCGCAAC CACTTCCGCT GTCAAGTCCA GTTCTACGGG CTCTCGGAGA
GGGGGCGTTG GTGAAGGCGA CAGTTCAGGT CAAGATGCCC GAGAGCCTCT
ATGACGAGTG GACCCAGGAT AGGGCCAAAC CCGTCACCCA GATCGTCAGC
TACTGCTCAC CTGGGTCCTA TCCCGGTTTG GGCAGTGGGT CTAGCAGTCG
GCCGAGGCCT GGGGTAGAGC AGACGCGGCC GCA
CGGCTCCGGA CCCCATCTCG TCTGCGCCGG CGT

**(SEQ ID 166)**

**Figure 19b**

K Y L L P T A A A G L L L L A A Q P
A M A K Q E V T Q I P A A L S V P E
G E N L V L N C S F T D S A I Y N L
Q W F R Q D P G K G L T S L L L I Q
S S Q R E Q T S G R L N A S L D K S
S G R S T L Y I A A S Q P G D S A T
Y L C A V R P T S G G S Y I P T F G
R G T S L I V H P Y I Q N P D P A V
Y Q L R D S K S S D K S V C L F T D
F D S Q T N V S Q S K D S D V Y I T
D K C V L D M R S M D F K S N S A V
A W S N K S D F A C A N A F N N S I
I P E D T F F P S P E S S M K K L L
F A I P L V V P F Y S H S A Q A G V
T Q T P K F Q V L K T G Q S M T L Q
C A Q D M N H E Y M S W Y R Q D P G
M G L R L I H Y S V G A G I T D Q G
E V P N G Y N V S R S T T E D F P L
R L L S A A P S Q T S V Y F C A S S
Y V G N T G E L F F G E G S R L T V
L E D L K N V F P P E V A V F E P S
E A E I S H T Q K A T L V C L A T G
F Y P D H V E L S W W V N G K E V H
S G V C T D P Q P L K E Q P A L N D
S R Y A L S S R L R V S A T F W Q D
P R N H F R C Q V Q F Y G L S E N D
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W G R A D A A A

**(SEQ ID 167)**

**Figure 20**

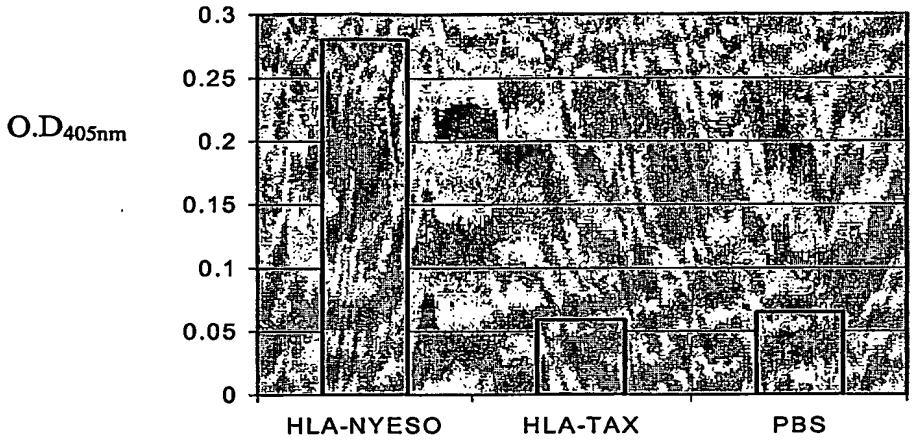

**Figure 21**

**DRA0101**

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 181 gtggatatgg caaagaagga gacggtctgg cggcttgaag aatttggacg atttgccagc
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**(SEQ ID 168)**

xxx - Fos Leucine zipper codons

xxx - Biotinylation tag codons

## Figure 22

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**(SEQ ID 169)**

 - Restriction enzyme sites

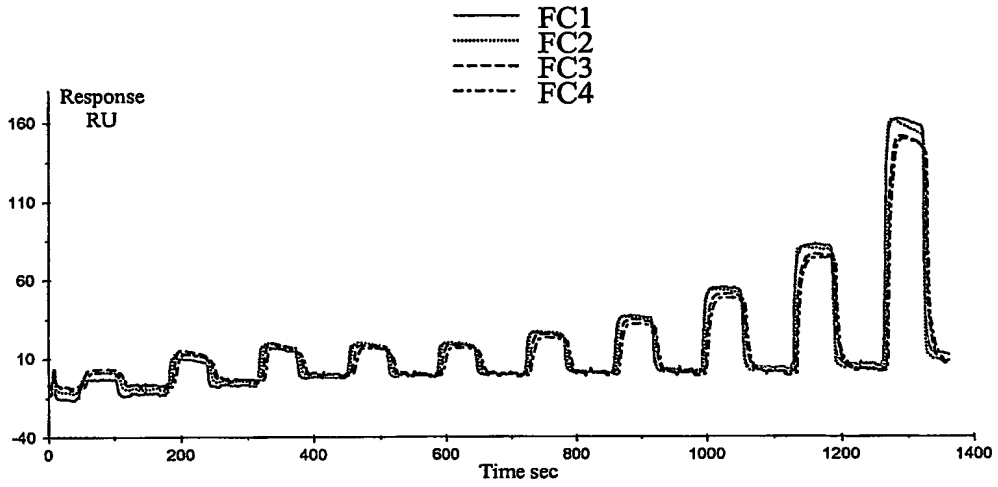
## Figure 23


**(SEQ ID 170)**

xxx - Jun Leucine zipper codons

xxx - HLA-loaded peptide

**Figure 24**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Time sec

**Figure 25**

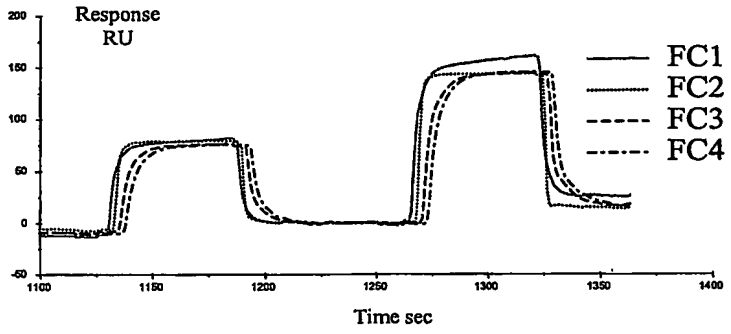
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**Figure 26**

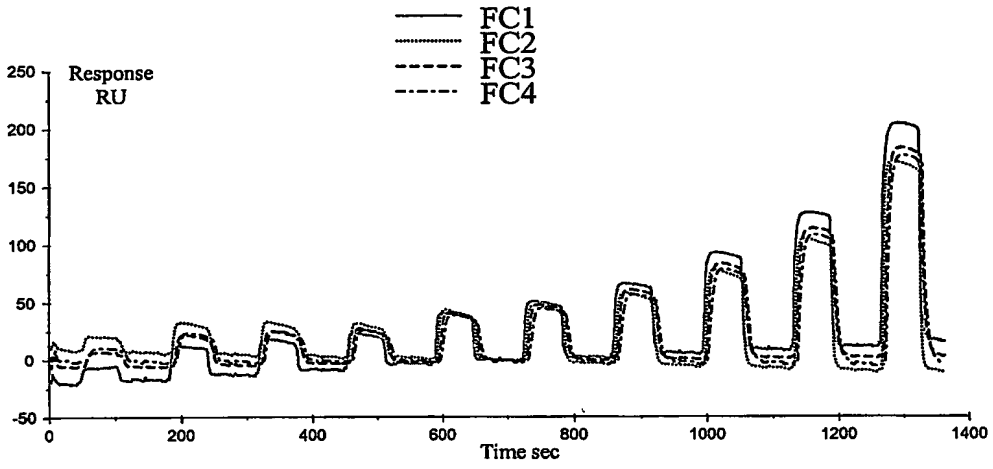
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**Figure 27**

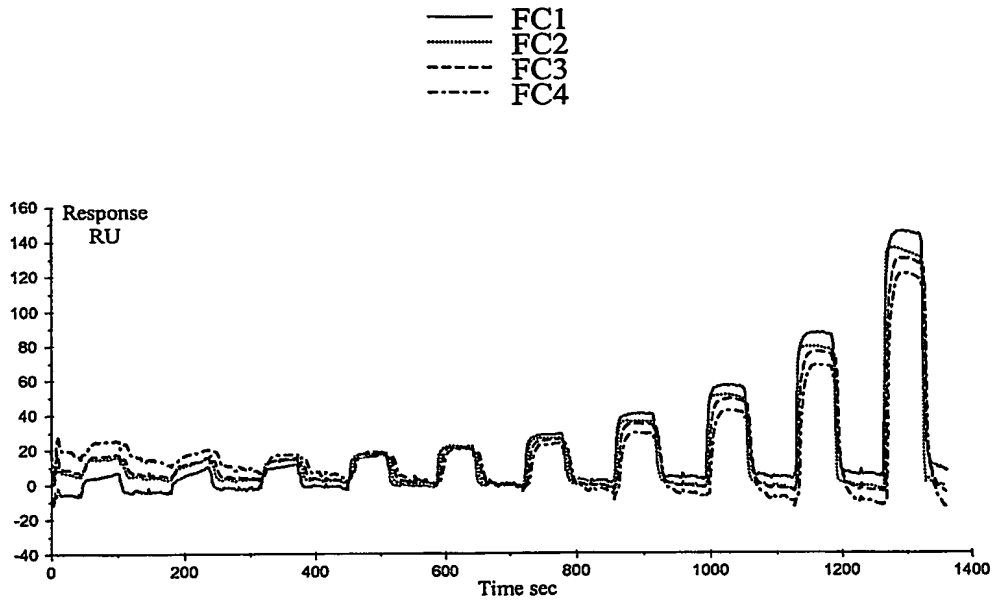
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**Figure 28**

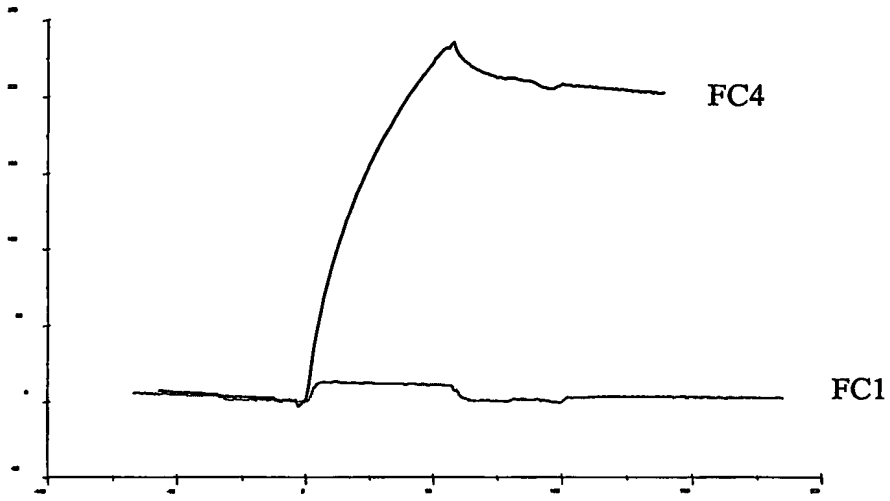


**Figure 29a**

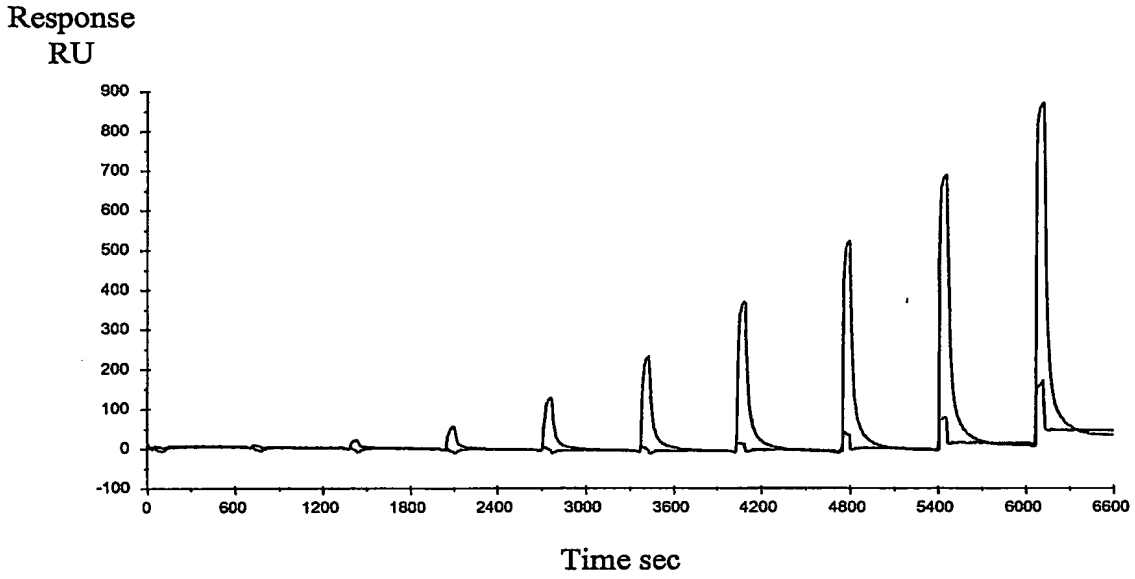
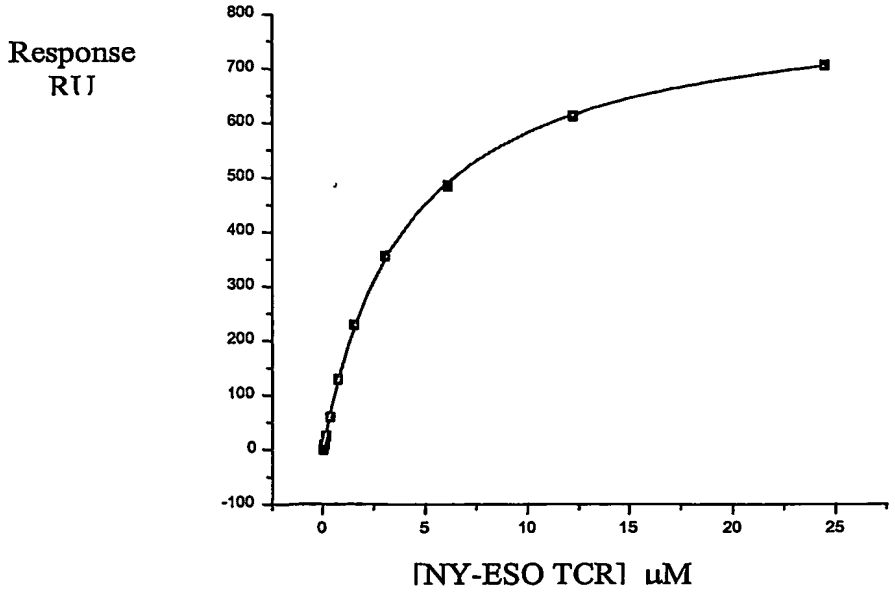



**Figure 29b**



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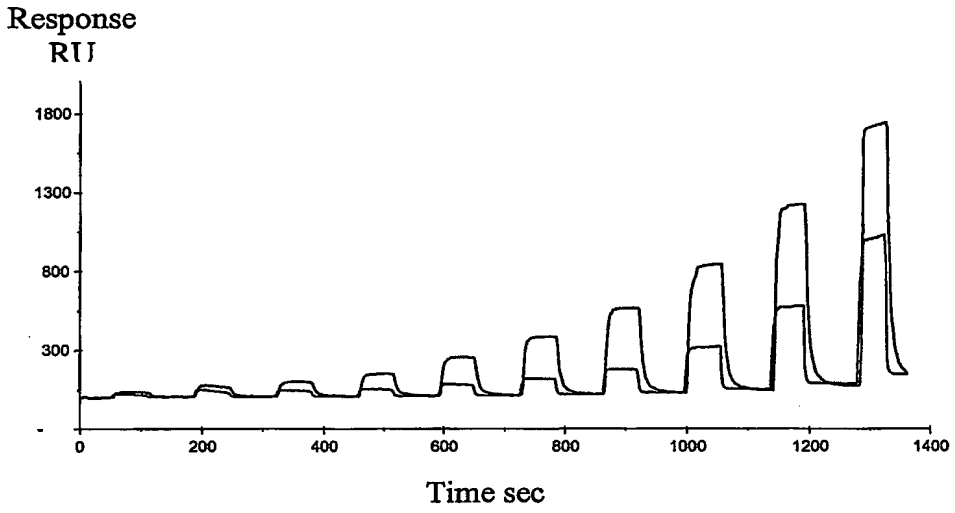



**Figure 30b**

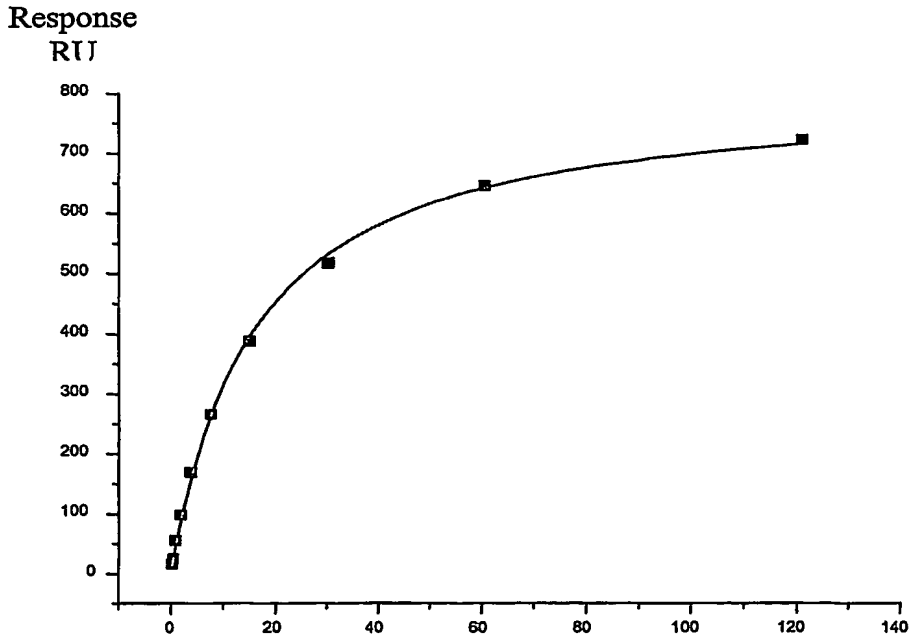


**Figure 31a**

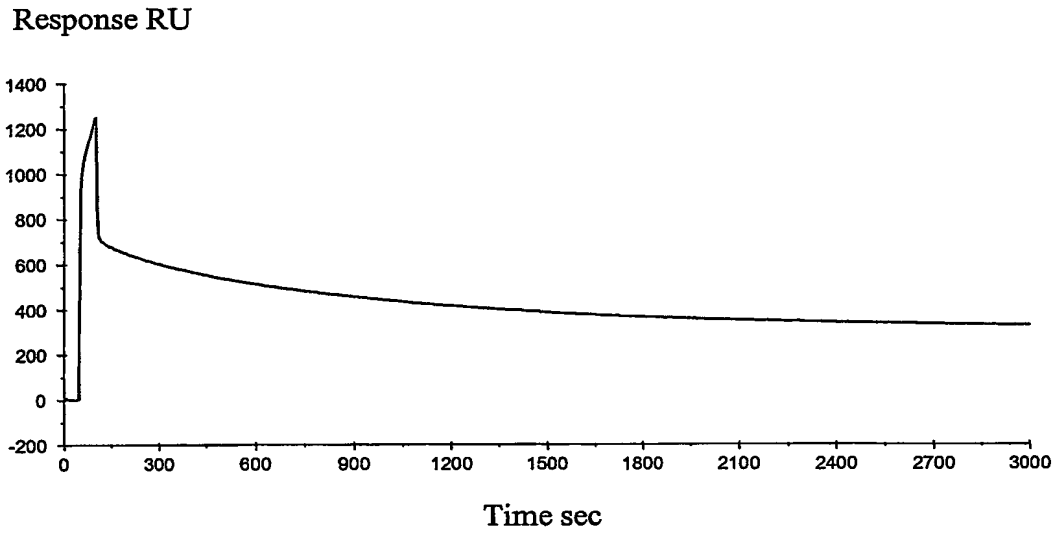



**Figure 31b**

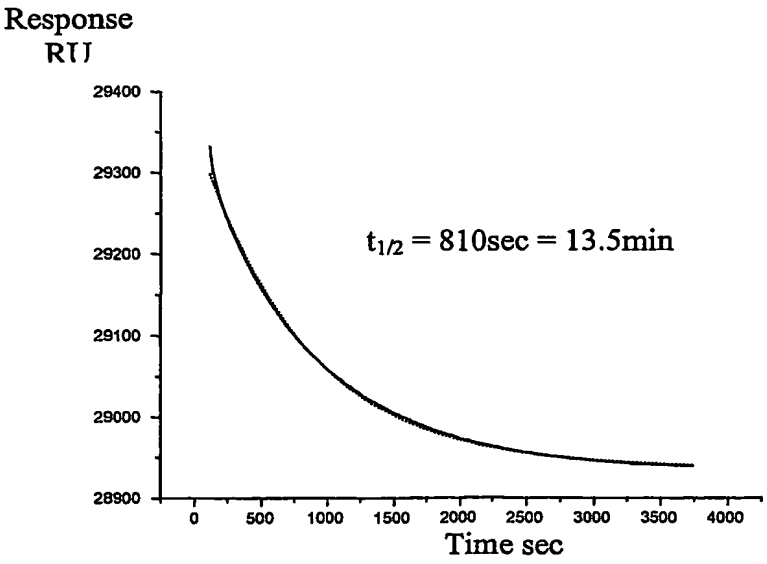


**Figure 32a**

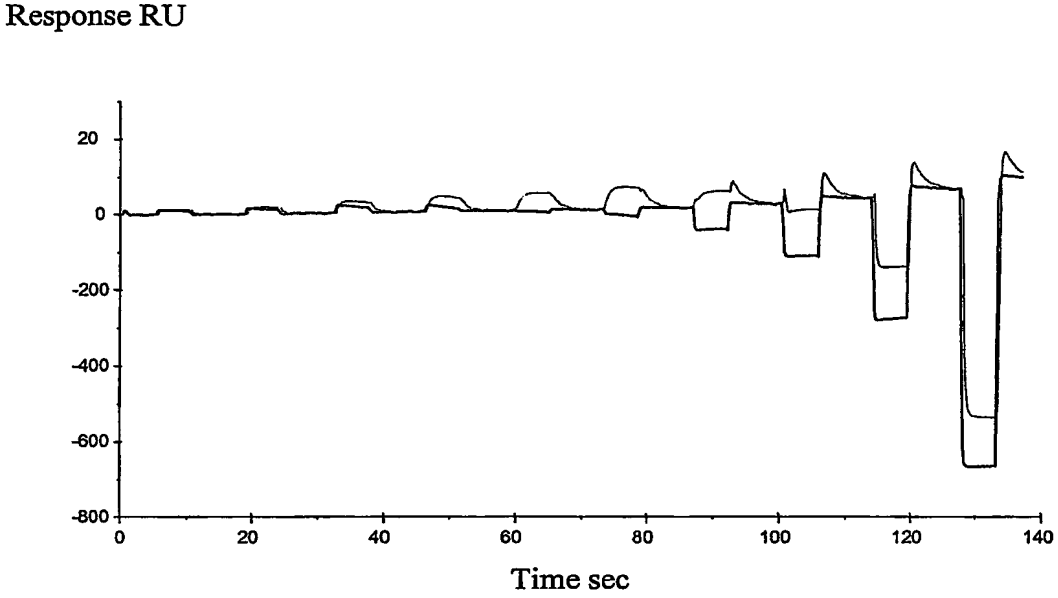



**Figure 32b**

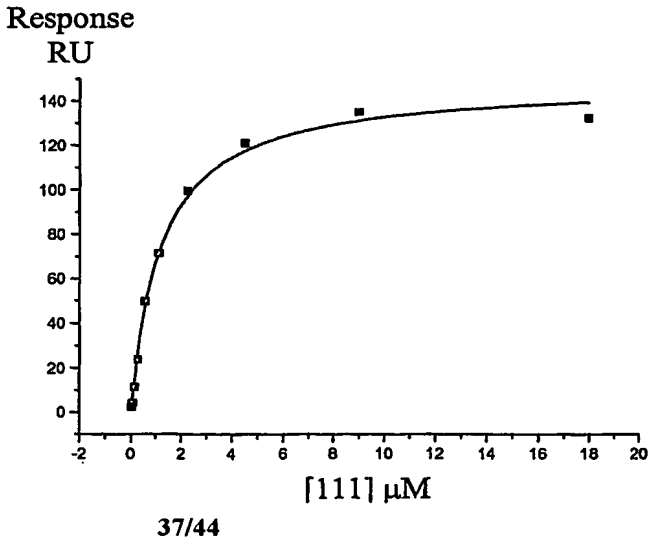


**Figure 33a**

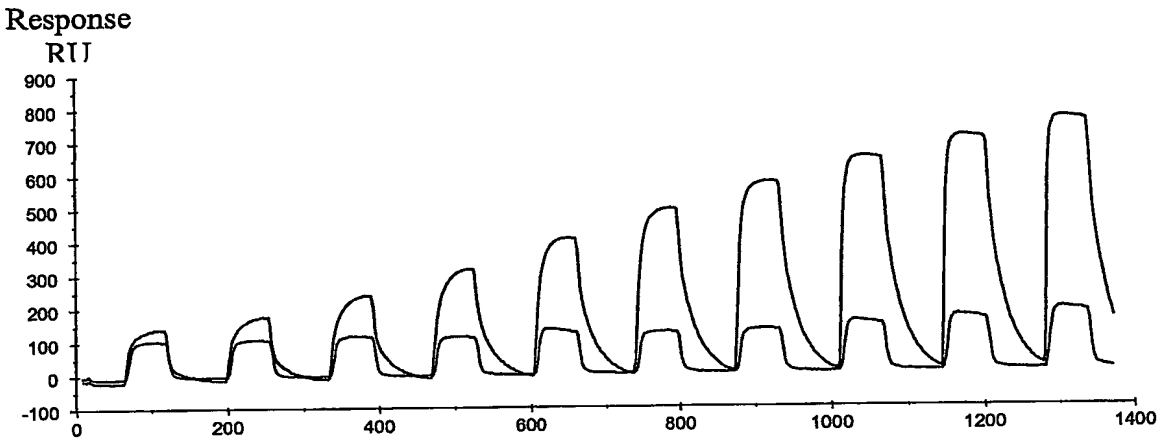



**Figure 33b**

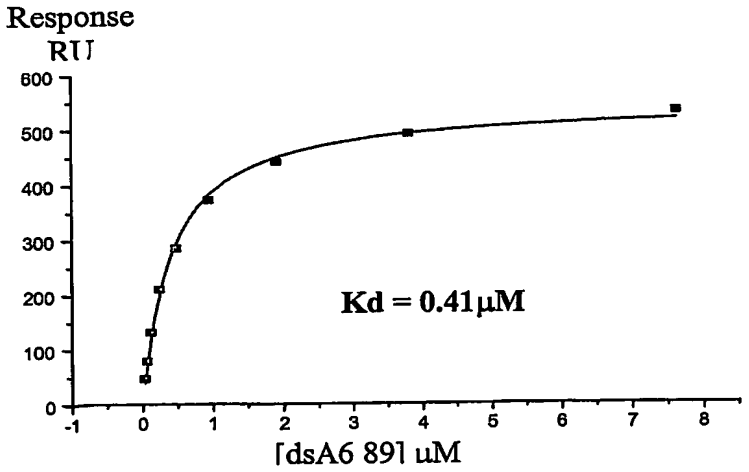


**Figure 34**

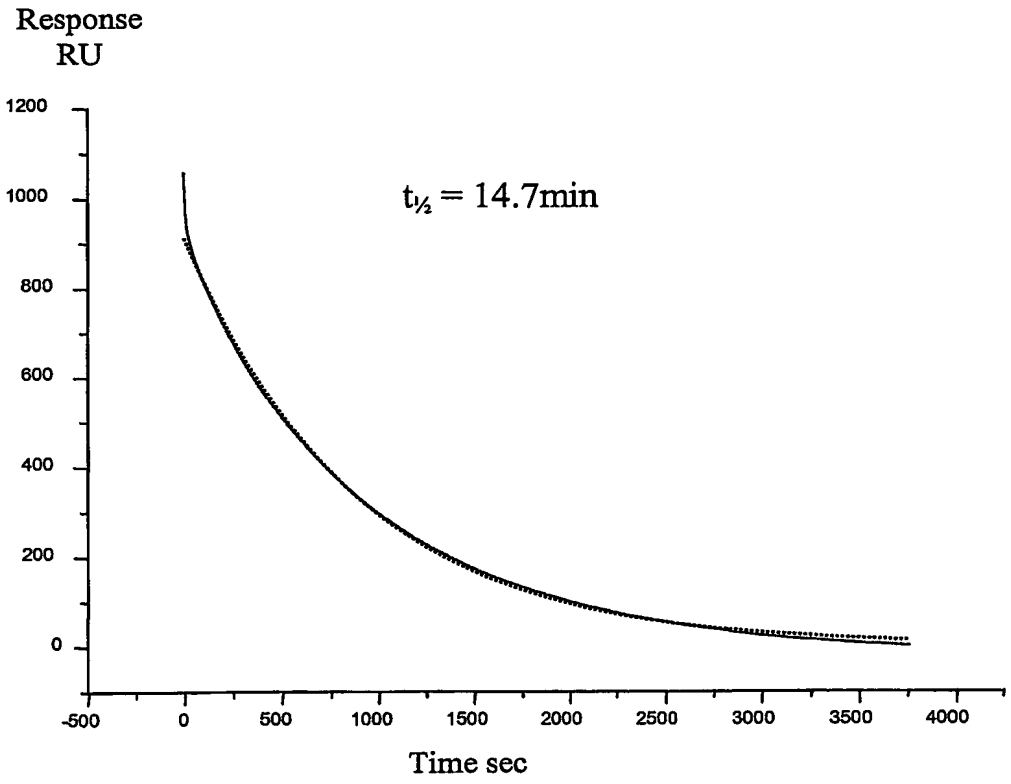

Response
RU
1200
1000
800
600
400
200
0
$t_{½}$ = 14.7min
-500
0
500
1000
1500
2000
2500
3000
3500
4000
Time sec

**Figure 35**

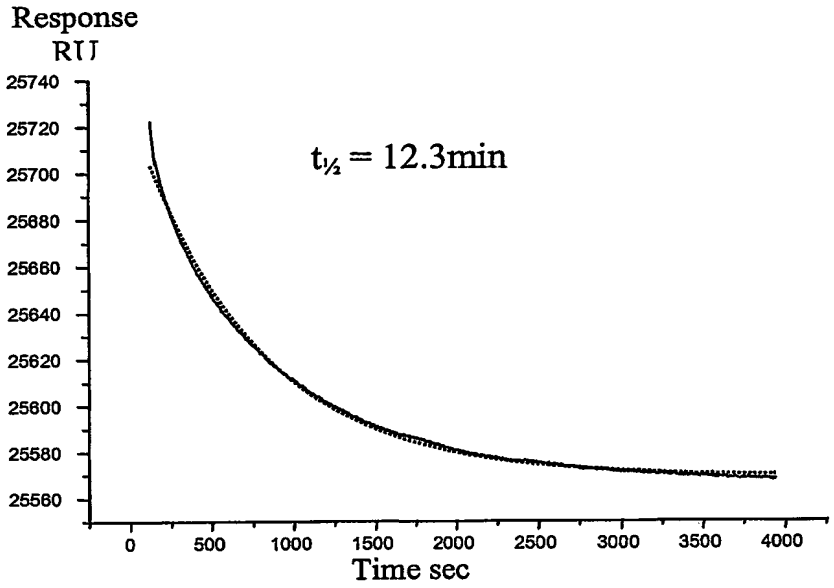
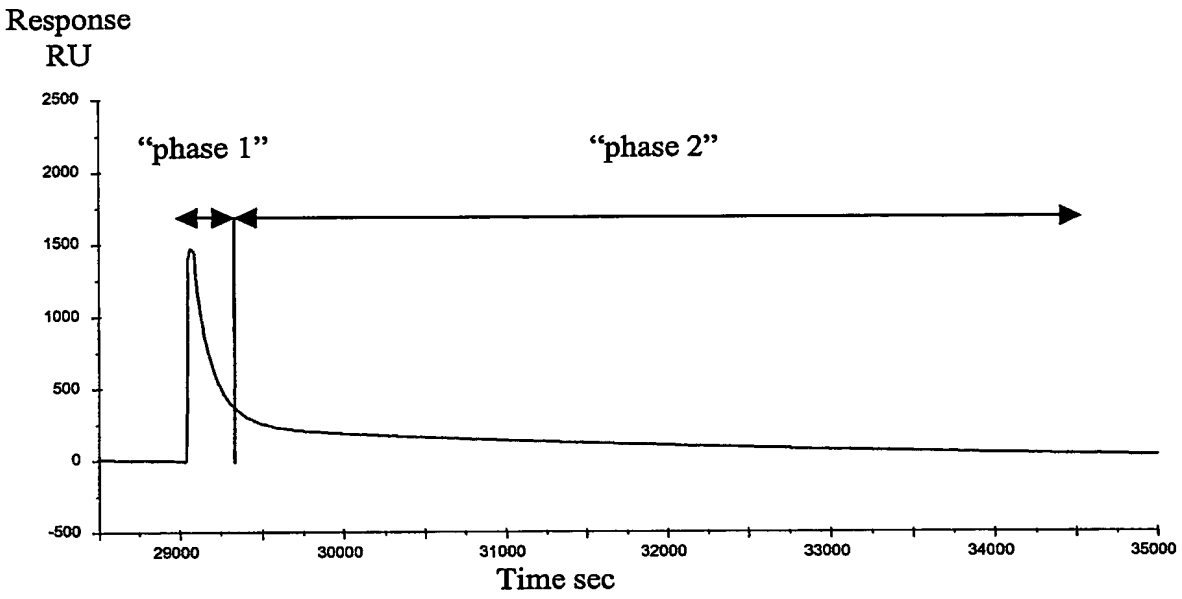
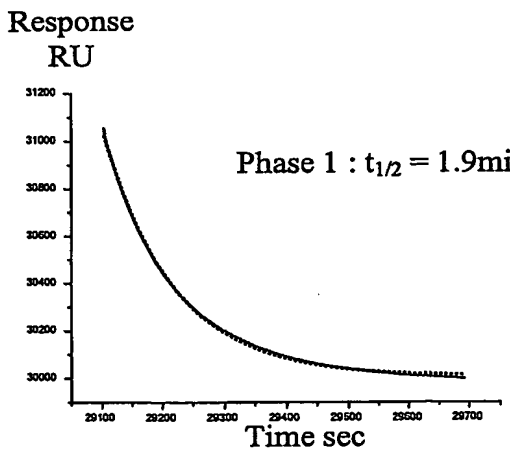

Response
RU
25740
25720
25700
25680
25660
25640
25620
25600
25580
25560
$t_{1/2}$ = 12.3min
0
500
1000
1500
2000
2500
3000
3500
4000
Time sec

**Figure 36**


Response
RU
2500
2000
1500
1000
500
0
-500
"phase 1"
"phase 2"
29000
30000
31000
32000
33000
34000
35000
Time sec


Response
RU
Phase 1 : $t_{1/2}$ = 1.9min
Time sec

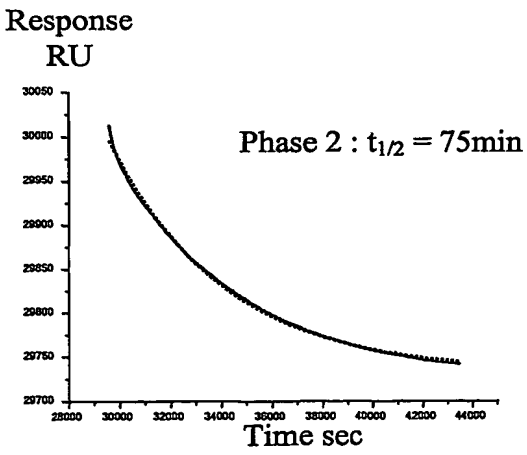

Response
RU
Phase 2 : $t_{1/2}$ = 75min
Time sec

Figure 37a

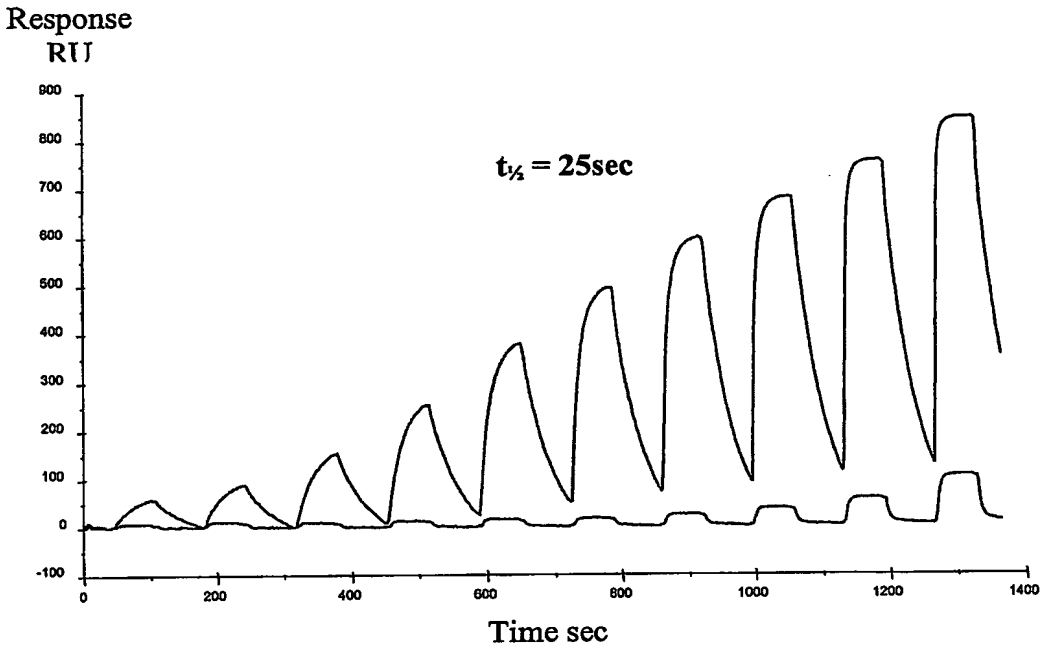



Figure 37b

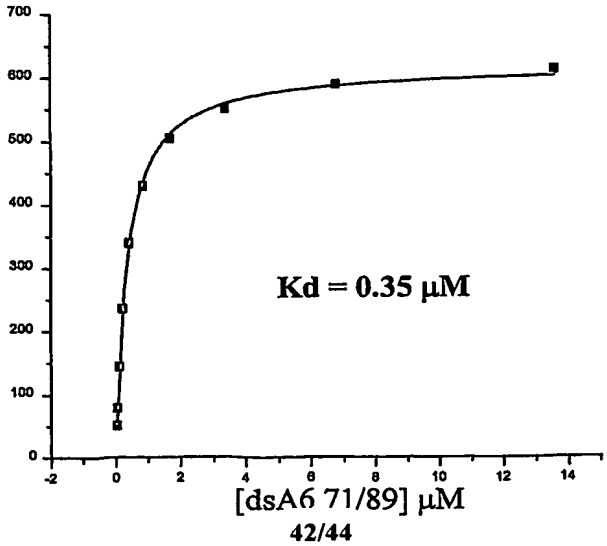


**Figure 38a**

MNAGVTQTPKF QVLKTGQSMT LQCAQDMNHE YMSWYRQDPG MGLRLIHYSV GAGITDQGEV PNGYNVSRST TEDFPLRLLS AAPSQTSVYF CASRPGLAGG RPEQYFGPGT RLTVT **(SEQ ID 171)**

**Figure 38b**

MNAGVTQTPKF QVLKTGQSMT LQCAQDMNHE YMSWYRQDPG MGLRLIHYSV GAGITDQGEV PNGYNVSRST TEDFPLRLLS AAPSQTSVYF CASRPGL**MSAX**PEQYFGPGT RLTVT **(SEQ ID 172)**

X denotes a position at which amino acids E, Q or R can be inserted.

**Figure 38c**

MNAGVTQTPKF QVLKTGQSMT LQCAQDMNHE YMSWYRQDPG MGLRLIHYSV GAGITDQGEV PNGYNVSRST TEDFPLRLLS AAPSQTSVYF CASRPGLAGG RPE**DQ**YFGPGT RLTVT **(SEQ ID 173)**

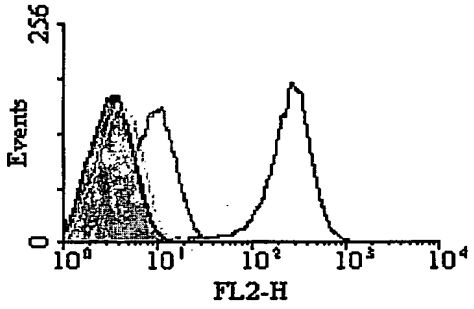
**Figure 38d**

MNAGVTQTPKF QVLKTGQSMT LQCAQDMNHE YMSWYRQDPG MGLRLIHYSV GAGITDQGEV PNGYNVSRST TEDFPLRLLS AAPSQTSVYF CASRPGL**VPG** RPEQ**Q**FGPGT RLTVT **(SEQ ID 174)**

**Figure 38e**

MNAGVTQTPKF QVLKTGQSMT LQCAQDMNHE YMSWYRQDPG MGLRLIHYSV GAGITDQGEV PNGYNVSRST TEDFPLRLLS AAPSQTSVYF CASRPGLAGG RP**HPQ**FGPGT RLTVT **(SEQ ID 175)**

Figure 39a



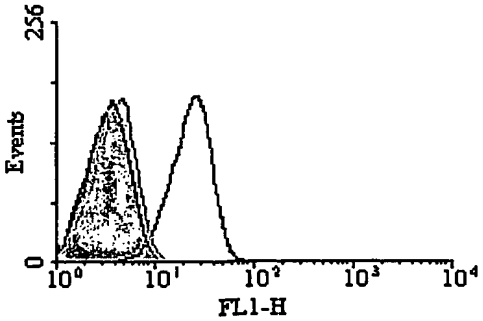

Unpulsed + A6(134)Tet-PE

Flu ($10^{-5}$M) + A6(134)Tet-PE

Tax ($10^{-5}$M) + A6(134)Tet-PE

Tax ($10^{-8}$M) + A6(134)Tet-PE

Tax ($10^{-9}$M) + A6(134)Tet-PE




Unpulsed + A6(134)Alexa 488

Flu ($10^{-5}$M) + A6(134)Alexa 488

Tax ($10^{-5}$M) + A6(134)Alexa 488

Tax ($10^{-8}$M) + A6(134)Alexa 488

Tax ($10^{-9}$M) + A6(134)Alexa 488

Figure 39b